

RESULT 1
 HSU44805
 LOCUS HSU44805 1979 bp DNA linear PRI 02-FEB-1996
 DEFINITION Human prostaglandin H synthase type 2 (PHS-2) gene, promoter
 sequence and partial cds.
 ACCESSION U44805
 VERSION U44805.1 GI:1174223
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1979)
 AUTHORS Kutchera,W.A., Jones,D.A., Matsunami,N., Groden,J., McIntyre,T.M.,
 Zimmerman,G.A., White,R.L. and Prescott,S.M.
 TITLE Prostaglandin H synthase-2 is expressed abnormally in human colon
 cancer: evidence for a transcriptional effect
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. (1996) In press
 REFERENCE 2 (bases 1 to 1979)
 AUTHORS Kutchera,W.A.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-1996) William A. Kutchera, Human Molecular
 Biology and Genetics, University of Utah, Building 533, Salt Lake
 City, UT 84112, USA
 FEATURES Location/Qualifiers
 source 1. .1979
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 promoter 1. .1976
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 CDS 1977. .>1979
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 /translation="M"

ORIGIN

Query Match 97.3%; Score 1851; DB 9; Length 1979;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1901; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATTCTAACATGGCTTCTAACCCTAACTAACATTAGTAGCTCTAACTATAAACTTCAAA 60
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 Db 46 GGATTCTAACATGGCTTCTAACCCTAACTAACATTAGTAGCTCTAACTATAAACTTCAAA 105
 Qy 61 TTTCAGTAGATGCAACCTACTCCTTTAAAATGAAACAGAAGATTGAAATTATTAAATTAT 120
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 Db 106 TTTCAGTAGATGCAACCTACTCCTTTAAAATGAAACAGAAGATTGAAATTATTAAATTAT 165

Qy	121	CAAAAAGAAAATGATCCACGCTCTTAGTTGAAATTTTCATGTAAGATTCCATGCAATAAAT	180
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Qy	181	AGGAGTGCCATAAATGGAATGATGAAATATGACTAGAGGAGGAGAAAGGCTTCCTAGATG	240
Db	226	AGGAGTGCCATAAATGGAATGATGAAATATGACTAGAGGAGGAGAAAGGCTTCCTAGATG	285
Qy	241	AGATGGAATTTTAGTCATCCGTGTCTCATGAAGAATCAGATGTGTACACTAAGCAAAACA	300
Db	286	AGATGGAATTTTAGTCATCCGTGTCTCATGAAGAATCAGATGTGTACACTAAGCAAAACA	345
Qy	301	GTTAAAAAAAACCTCCAAGTGAGTCTCTTATTTATTTTTTTCTTATAAGACTTCTACA	360
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Qy	361	AATTGAGGTACCTGGTGTAGTTTTATTTTCAGGTTTTATGCTGTCATTTTCCTGTAATGCT	420
Db	406	AATTGAGGTACCTGGTGTAGTTTTATTTTCAGGTTTTATGCTGTCATTTTCCTGTAATGCT	465
Qy	421	AAGGACTTAGGACATAACTGAATTTTCTATTTTCCACTTCTTTTCTGGTGTGTGTGTATA	480
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Qy	481	TATATATGTATATATACACACACACATATACATATATATATTTTTTAGTATCTCACCTCA	540
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Qy	601	AACTGTTAAATCTCCCTTCCATCTAATTAATTCCTCATCCAACATGTTCCAAAACGAG	660
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Qy	661	AATAGAAAATTAGCCCCAATAAGCCCAGGCAACTGAAAAGTAAATGCTATGTTGTACTTT	720
Db	706	AATAGAAAATTAGCCCCAATAAGCCCAGGCAACTGAAAAGTAAATGCTATGTTGTACTTT	765
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Qy	781	TTAAAACCTCGAATTTATTTTACCAGTATCTCCTATGAAGGGCTAGTAACCAAATAATCC	840
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Qy	841	ACGCATCAGGGAGAGAAATGCCTTAAGGCATACGTTTTGGACATTTAGCGTCCCTGCAA	900
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Qy	901	TTCTGGCCATCGCCGCTTCCTTTGTCCATCAGAAGGCAGGAACTTTATATTGGTGACCC	960
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Qy	961	GTGGAGCTCACATTAACATTTTACAGGGTAACTGCTTAGGACCAGTATTATGAGGAGGAT	1020

Db	1006	GTGGAGCTCACATTAACCTATTTACAGGGTAACTGCTTAGGACCAGTATTATGAGGAGAAT	1065
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Db	1066	TTACCTTTCCCGCCTCTCTTTCCAAGAAACAAGGAGGGGGTGAAGGTACGGAGAACAGTA	1125
Qy	1081	TTTCTTCTGTTGAAAGCAACTTAGCTACAAAGATAAATTACAGCTATGTACACTGAAGGT	1140
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Qy	1141	AGCTATTTTCATTCCACAAAATAAGAGTTTTTTAAAAAGCTATGTATGTATGTCCTGCATA	1200
Db	1186	AGCTATTTTCATTCCACAAAATAAGAGTTTTTTAAAAAGCTATGTATGTATGTCCTGCATA	1245
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Qy	1261	TTAACCTTACTCGCCCCAGTCTGTCCCGACGTGACTTCCTCGACCCTCTAAAGACGTACA	1320
Db	1306	TTAACCTTACTCGCCCCAGTCTGTCCCGACGTGACTTCCTCGACCCTCTAAAGACGTACA	1365
Qy	1321	GACCAGACACGGCGGGCGGGCGGGAGAGGGGATTCCCTGCGCCCCCGGACCTCAGGGCC	1380
Db	1366	GACCAGACACGGCGGGCGGGCGGGAGAGGGGATTCCCTGCGCCCCCGGACCTCAGGGCC	1425
Qy	1381	GCTCAGATTCTTGAGAGGAAGCCAAGTGTCTTCTGCCCTCCCCCGGTATCCCATCCAA	1440
Db	1426	GCTCAGATTCTTGAGAGGAAGCCAAGTGTCTTCTGCCCTCCCCCGGTATCCCATCCAA	1485
Qy	1441	GGCGATCAGTCCAGAACTGGCTCTCGGAAGCGCTCGGGCAAAGACTGCGAAGAAGAAAAG	1500
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Qy	1501	ACATCTGGCGGAAACCTGTGCGCCTGGGGCGGTGGAACCTCGGGGAGGAGAGGGAGGGATC	1560
Db	1546	ACATCTGGCGGAAACCTGTGCGCCTGGGGCGGTGGAACCTCGGGGAGGAGAGGGAGGGATC	1605
Qy	1561	AGACAGGAGAGTGGGGACTACCCCTCTGCTCCCAAATTGGGGCAGCTTCTGGGTTTCC	1620
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Qy	1621	GATTTTCTCATTTCCGTGGGTAAAAAACCTGCCCCACCGGGCTTACGCAATTTTTTTTA	1680
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Qy	1681	AGGGGAGAGGAGGGGAAAAATTTGTGGGGGGTACGAAAAGGCGGAAAGAAACAGTCATTTT	1740
Db	1726	AGGGGAGAGGAGGGGAAAAATTTGTGGGGGGTACGAAAAGGCGGAAAGAAACAGTCATTTT	1785
Qy	1741	GTCACATGGGCTTGGTTTTTCAGTCTTATAAAAAGGAAGGTTCTCTCGGTTAGCGACCAAT	1800
Db	1786	GTCACATGGGCTTGGTTTTTCAGTCTTATAAAAAGGAAGGTTCTCTCGGTTAGCGACCAAT	1845
Qy	1801	TGTCATACGACTTGACAGTGAGCGTCAGGAGCACGTCCAGGAACCTCCTCAGCAGCGCCTCC	1860

Db 1846 TGTACATACGACTTGTCAGTGAGCGTCAGGAGCACGTCCAGGAACTCCTCAGCAGCGCCTCC 1905

Qy 1861 TTCAGCTCCACAGCCAGACGCCCTCAGACAGCAAAGCCTACC 1902

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Db 1906 TTCAGCTCCACAGCCAGACGCCCTCAGACAGCAAAGCCTACC 1947